

SCORE Search Results Details for Application 10529592 and Search Result 20090427_122917_us-10-529-592a-1.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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This page gives you Search Results detail for the Application 10529592 and Search Result 20090427_122917_us-10-529-592a-1.rst.

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GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2009, 04:16:35 ; Search time 1875 Seconds
(without alignments)
45457.283 Million cell updates/sec

Title: US-10-529-592A-1
Perfect score: 881
Sequence: 1 gggccatgacccccgctgct.....aaataaagatcctctgtaac 881

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 83780570 seqs, 48372533981 residues

Total number of hits satisfying chosen parameters: 167561140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*

9: gb_est9:*
 10: gb_est10:*
 11: gb_est11:*
 12: gb_est12:*
 13: gb_est13:*
 14: gb_est14:*
 15: gb_est15:*
 16: gb_est16:*
 17: gb_est17:*
 18: gb_est18:*
 19: gb_gss1:*
 20: gb_gss2:*
 21: gb_gss3:*
 22: gb_gss4:*
 23: gb_gss5:*
 24: gb_gss6:*
 25: gb_gss7:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	710.6	80.7	979	5	BQ672221			BQ672221 AGENCOURT
	2	703	79.8	916	5	BU527159			BU527159 AGENCOURT
	3	685.6	77.8	735	4	BI914593			BI914593 603179545
	4	650.4	73.8	889	5	BQ671560			BQ671560 AGENCOURT
	5	563	63.9	586	3	BE875115			BE875115 601485988
c	6	549	62.3	687	4	BM977476			BM977476 UI-CF-EN1
c	7	547.4	62.1	677	4	BQ045152			BQ045152 UI-CF-EN1
	8	545.6	61.9	840	4	BI546970			BI546970 603190185
	9	545.4	61.9	838	7	CF993841			CF993841 AGENCOURT
c	10	543.8	61.7	600	1	AA760709			AA760709 nz13c11.s
c	11	539.8	61.3	573	4	BQ025351			BQ025351 UI-1-BB1p
c	12	539.8	61.3	581	4	BQ025360			BQ025360 UI-1-BB1p
	13	536.4	60.9	591	4	BM711587			BM711587 UI-E-CL1-
c	14	536	60.8	539	1	AI973037			AI973037 wr46g08.x
	15	530.2	60.2	843	7	CB993691			CB993691 AGENCOURT
	16	510.2	57.9	577	5	BQ425608			BQ425608 AGENCOURT
c	17	501.4	56.9	541	4	BQ025279			BQ025279 UI-1-BB1p
	18	501.2	56.9	542	4	BM688675			BM688675 UI-E-CQ1-
c	19	491	55.7	495	2	AW072412			AW072412 xa07f07.x
c	20	486.4	55.2	491	1	AI969836			AI969836 wq75f01.x
	21	474	53.8	474	4	BM725994			BM725994 UI-E-EJ0-
	22	472.4	53.6	788	7	CD101714			CD101714 AGENCOURT

	23	460.6	52.3	593	18	W56389	W56389	zc57b01.r1
c	24	453	51.4	456	1	AI824062	AI824062	wj35f10.x
c	25	452.4	51.4	469	4	BM681000	BM681000	UI-E-EJ0-
c	26	447.4	50.8	460	1	AI201581	AI201581	qc02g09.x
	27	438.4	49.8	443	8	CN366258	CN366258	170006008
c	28	434.8	49.4	456	5	BU727045	BU727045	UI-E-CQ1-
	29	433	49.1	447	7	CD674248	CD674248	fs08d06.y
c	30	417.6	47.4	439	2	AW779356	AW779356	hn80b03.x
	31	417	47.3	626	4	BM688212	BM688212	UI-E-CL0-
	32	416.2	47.2	803	7	CB998149	CB998149	AGENCOURT
c	33	404.8	45.9	412	1	AI042370	AI042370	ox62b07.x
c	34	404	45.9	429	1	AA827147	AA827147	ob53c05.s
	35	397	45.1	398	5	BX096382	BX096382	BX096382
	36	383.6	43.5	413	1	AA490346	AA490346	aa44a05.r
c	37	380	43.1	381	1	AI221443	AI221443	qg75c09.x
	38	372.8	42.3	616	3	BG285710	BG285710	602380756
	39	367	41.7	574	18	W37398	W37398	zc11a10.r1
c	40	360	40.9	365	2	AW419070	AW419070	ha17c11.x
c	41	357.4	40.6	361	2	AW439942	AW439942	ha11e11.x
c	42	356.4	40.5	384	5	BU726946	BU726946	UI-E-CL0-
c	43	351.4	39.9	366	1	AI216467	AI216467	qh07h08.x
c	44	351.2	39.9	386	18	N98734	N98734	zb87f07.s1
	45	338.4	38.4	1094	4	BM925906	BM925906	AGENCOURT

ALIGNMENTS

RESULT 1

BQ672221

LOCUS BQ672221 979 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT_8303632 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6274816
5', mRNA sequence.

ACCESSION BQ672221

VERSION BQ672221.1 GI:21783055

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 979)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2456 row: p column: 17
 High quality sequence stop: 550.

FEATURES Location/Qualifiers
 source 1. .979
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6274816"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 80.7%; Score 710.6; DB 5; Length 979;
 Best Local Similarity 97.3%; Pred. No. 1.7e-163;
 Matches 786; Conservative 0; Mismatches 15; Indels 7; Gaps 6;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	23	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	82
Qy	61	CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	83	CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	142
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	143	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	202
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	203	TGCCTGAAAGGCTTTCAAATGTGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	262
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCCGACATCATCATCACGCCCCCACCACCCACG	300
Db	263	GTCCTGAACGACAAGCACCTGGACGTGCCCCGACATCATCATCACGCCCCCACCACCCACG	322

Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	323	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	382
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	383	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	442
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	443	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	502
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAA-CCCGGGCCTCCGCTCAGAGAGACGTGGCAG	539
Db	503	CTGAATACCCTGGATGGGAACTGAGCGAACCCCGGGCCTCCGCTCAGAGAGACGTGGCAG	562
Qy	540	GACCAGCGAGGAATCCAGCCTGTCCA-CTTCCAGAACAGTGTTTCCAGGCCCGCTGAG	598
Db	563	GACCAGCGAGGAATCCAGCCTGTCCACCTTCCAGAACAGTGTTTCCAGGCCCGCTGAG	622
Qy	599	TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGC	658
Db	623	TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGNTGAAAGGGAGCGC	682
Qy	659	CATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCT-CTTCTGGACAAACACACCC-TC	716
Db	683	CATGGTCCTGGCTGGTGGGGTCCCAGGGAGAGGCTCTCCTTCTGGACAAACACACCCTTC	742
Qy	717	CCAGCCCCCAGGGCTGTGCAAACACATG-CCCCTGCCATAAGCACCAACAAGAAC--TTC	773
Db	743	CCAGCCCCCAGGGCTGTGCAAACACATGCCCCCGGCCATAAGCCCCCACAAAACCTTCT	802
Qy	774	TTGCAGGTGGAGTGGCTGTTTTTTTATAA	801
Db	803	TGGCCGGGGGAAGGGCTTTTTTTTTTTAA	830

RESULT 2

BU527159

LOCUS BU527159 916 bp mRNA linear EST 13-SEP-2002

DEFINITION AGENCOURT_10154878 NIH_MGC_101 Homo sapiens cDNA clone

IMAGE:6536921 5', mRNA sequence.

ACCESSION BU527159

VERSION BU527159.1 GI:22837600

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 916)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2699 row: a column: 17
High quality sequence stop: 653.
FEATURES Location/Qualifiers
source 1. .916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536921"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 79.8%; Score 703; DB 5; Length 916;
Best Local Similarity 96.9%; Pred. No. 1.2e-161;
Matches 749; Conservative 0; Mismatches 20; Indels 4; Gaps 3;

Qy	1	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	3	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	62
Qy	61	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	63	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	122
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180

http://es/ScoreAccessWeb/GetItem.action?AppId=1052959...27_122917_us-10-529-592a-1.rst&ItemType=4&startByte=0 (7 of 35)5/19/2009 9:51:32 AM

ACCESSION

BI914593

VERSION

BI914593.1 GI:16178714

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 735)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM11614 row: j column: 11

High quality sequence stop: 723.

FEATURES

Location/Qualifiers

source

1. .735

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5243626"

/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match

77.8%; Score 685.6; DB 4; Length 735;

Best Local Similarity

96.6%; Pred. No. 2.3e-157;

Matches 730; Conservative 0; Mismatches 4; Indels 22; Gaps 2;

Qy

119

GCAGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGT

178

|||||

Db	1	GCAGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGT	60
Qy	179	CCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCC	238
Db	61	CCTGCCTGAAA-----TGCAGCAGCAGCAGCCACGACGAGGCCC	99
Qy	239	CCGTCCTGAACGACAAGCACCTGGACGTGCCCACATCATCATCACGCCCCCACC	298
Db	100	CCGTCCTGAACGACAAGCACCTGGACGTGCCCACATCATCATCACGCCCCCACC	159
Qy	299	CGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGT	358
Db	160	CGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGT	219
Qy	359	GCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCT	418
Db	220	GCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCT	279
Qy	419	GGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTG	478
Db	280	GGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTG	339
Qy	479	TGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCA	538
Db	340	TGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCA	399
Qy	539	GGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAG	598
Db	400	GGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAG	459
Qy	599	TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGC	658
Db	460	TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGC	519
Qy	659	CATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCC	718
Db	520	CATGGTCCTGGCTGTTGGGGTCCCAGGCAGAGGCTCTCTTCTGGACAAACACACCCTCCC	579
Qy	719	AG-CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGC	777
Db	580	AGCCCCCAGGGCTGTGCAAACACATGCCCCTCCCATAAGCACCAACAAGAACTTCTTGC	639
Qy	778	AGGTGGAGTGGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGA	837
Db	640	AGGTGGAGTGGCTGTATTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGA	699
Qy	838	TTTATAATTTCTTTTTTGCATTATAAATAAAGATCC	873
Db	700	TTTATAATTTCTTTTTTGCATTATAAATAAAGATCC	735

RESULT 4

BQ671560

LOCUS BQ671560 889 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT_8171941 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6277428 5', mRNA sequence.

ACCESSION BQ671560

VERSION BQ671560.1 GI:21782394

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 889)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2463 row: m column: 13

High quality sequence stop: 549.

FEATURES Location/Qualifiers

source 1. .889

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6277428"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_102"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.8%; Score 650.4; DB 5; Length 889;
 Best Local Similarity 93.1%; Pred. No. 1.1e-148;
 Matches 715; Conservative 0; Mismatches 46; Indels 7; Gaps 3;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	23	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	82
Qy	61	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	83	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	142
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	143	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	202
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	203	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	262
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCCGACATCATCATCACGCCCCCACCACG	300
Db	263	GTCCTGAACGACAAGCACCTGGACGTGCCCCGACATCATCATCACGCCCCCACCACG	322
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	323	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	382
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	383	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	442
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	443	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	502
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG	540
Db	503	CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG	562
Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGG-CCCCGCTGAGT	599
Db	563	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAGG	622
Qy	600	GGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCC	659
Db	623	GGACCGGACCTCTGACACCTCCCGGTTCTTGCTGACTCCGGCCTGGGGAAAGGGAACCGC	682
Qy	660	ATGGTCC--TGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCC	717

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      ||||| | | ||| ||||| ||| | | ||| || | |||
Db      683 TTGGTCCCTGGCTGTTGGGGGGCCCAGGGAAAGGGTCGTCTTCGGAGCAAACGAACCTTT 742

Qy      718 CA----GCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACC 761
      | |||| | | ||| | | ||| | | ||| | |||
Db      743 GAAAGCCCCCCCCGGGCATGGACAAAACAAGCCCCCGGTCCTATGGACC 790

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RESULT 5

BE875115

LOCUS BE875115 586 bp mRNA linear EST 20-OCT-2000

DEFINITION 601485988F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888621 5',
mRNA sequence.

ACCESSION BE875115

VERSION BE875115.1 GI:10323891

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 586)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:<http://image.llnl.gov>

Plate: LLAM9668 row: o column: 22

High quality sequence stop: 586.

FEATURES

Location/Qualifiers

source

1. .586

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3888621"

/tissue_type="large cell carcinoma, undifferentiated"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_69"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 63.9%; Score 563; DB 3; Length 586;
Best Local Similarity 99.0%; Pred. No. 3.4e-127;
Matches 577; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	300	GGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTG	359
Db	1	GGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTG	60
Qy	360	CCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTG	419
Db	61	CCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTG	120
Qy	420	GCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGT	479
Db	121	GCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGT	180
Qy	480	GCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAG	539
Db	181	GCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAG	240
Qy	540	GACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAGT	599
Db	241	GACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAGT	300
Qy	600	GGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCC	659
Db	301	GGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCC	360
Qy	660	ATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCA	719
Db	361	ATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCA	420
Qy	720	GCCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAG	779
Db	421	GCCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAG	480
Qy	780	GTGGAGTGGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATT	839
Db	481	GTGGAGTGGCTGTTTTTTTATAAGTCGTTTTACAGATACGGAAACAGTCCAAAATGGGATT	540
Qy	840	TATAATTTCTTTTTTGCATTA-TAAATAAAGATCCTCTGTAAC	881
Db	541	TATAATTTCTTTTTTGCATTACTCAAGATCCTCTGTAAC	583

RESULT 6
BM977476/c

LOCUS BM977476 687 bp mRNA linear EST 21-FEB-2003
 DEFINITION UI-CF-EN1-aee-b-14-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-aee-b-14-0-UI 3', mRNA sequence.
 ACCESSION BM977476
 VERSION BM977476.1 GI:19595931
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 687)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.
 FEATURES Location/Qualifiers
 source 1..687
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-aee-b-14-0-UI"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EN1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT. TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h TAG_LIB=UI-CF-EN1 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 62.3%; Score 549; DB 4; Length 687;
 Best Local Similarity 100.0%; Pred. No. 9.6e-124;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	333	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	392
Db	575	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	516
Qy	393	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	452
Db	515	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	456
Qy	453	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC	512
Db	455	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC	396
Qy	513	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	572
Db	395	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	336
Qy	573	AACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	632
Db	335	AACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	276
Qy	633	GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	692
Db	275	GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	216
Qy	693	TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCC	752
Db	215	TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCC	156
Qy	753	ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA	812

Db 155 ATAAGCACCAACAAGAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 96

Qy 813 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 872
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Db 95 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 36

Qy 873 CTCTGTAAAC 881
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Db 35 CTCTGTAAAC 27

RESULT 7

BQ045152/c

LOCUS BQ045152 677 bp mRNA linear EST 21-FEB-2003

DEFINITION UI-CF-EN1-ael-o-16-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-ael-o-16-0-UI 3', mRNA sequence.

ACCESSION BQ045152

VERSION BQ045152.1 GI:19796231

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 677)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES Location/Qualifiers

source 1..677

/organism="Homo sapiens"


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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-ael-o-16-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

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ORIGIN

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Query Match          62.1%;   Score 547.4;   DB 4;   Length 677;
Best Local Similarity 99.8%;   Pred. No. 2.4e-123;
Matches 548;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

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Qy      333 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      564 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 505

Qy      393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      504 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 445

Qy      453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      444 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 385

Qy      513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      384 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 325

Qy      573 AACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632

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Db      324 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 265

Qy      633 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      264 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 205

Qy      693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCCTGCC 752
      ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      204 TCTCTTTTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCCTGCC 145

Qy      753 ATAAGCACCAACAAGAAGTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTTACA 812
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      144 ATAAGCACCAACAAGAAGTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTTACA 85

Qy      813 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 872
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      84 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 25

Qy      873 CTCTGTAAAC 881
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Db      24 CTCTGTAAAC 16
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RESULT 8

BI546970

LOCUS BI546970 840 bp mRNA linear EST 05-SEP-2001

DEFINITION 603190185F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261660 5',
mRNA sequence.

ACCESSION BI546970

VERSION BI546970.1 GI:15434282

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 840)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11659 row: i column: 21
 High quality sequence stop: 737.

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5261660"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_95"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.5 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

ORIGIN

Query Match 61.9%; Score 545.6; DB 4; Length 840;
 Best Local Similarity 89.1%; Pred. No. 6.8e-123;
 Matches 709; Conservative 0; Mismatches 34; Indels 53; Gaps 9;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	49	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	108
Qy	61	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	109	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	168
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	169	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	228
Qy	181	TGCCTGAAAG-----GCTTTCAA	198
Db	229	TGCCTGAAAGACGCCGTTTTTCATCTGTGATGCGGGACAGCTGCGCTCCTTGCTGCGAG	288
Qy	199	ATGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCTGAACGACAAGCAC	258
Db	289	GCGTCAGGACCCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCTGAACGACAAGCAC	348

Qy	259	CTGGACGTGCCCCGACATCATCATCACGCCCCCCCACCCCCACGGGCATGATGCTGCCGAGG	318
Db	349	CTGGACGTGCCCCGACATCATCATCACGCCCCCA-CCCCACGGGCATGATGCTGCCGAGG	407
Qy	319	GACTTGGGGAGCACAGTCTGGCTGG-ATGAGACAGGGTCGTGCCCAGATGATGGAGAAAT	377
Db	408	GACTTGGGGAGCACAGTCTGGCTGGCATGAGACAGGGTCGTGCCCAGATGATGGAGAAAT	467
Qy	378	CGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCC	437
Db	468	CGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCC	527
Qy	438	CGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGG	497
Db	528	CGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGG	587
Qy	498	GAAC-TGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCA	556
Db	588	GAAC TTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCA	647
Qy	557	GCCTGTCCACTTCCAGAA-CAGTGTTTCCCAGGCCCGCTG-AGTGGACCGGACCTC-TG	613
Db	648	GCCTGTCCACTTCCAGAACCAGTGTTTACAGGCCCGCTGAAGTGGACCGGACCTCTTG	707
Qy	614	ACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGT	673
Db	708	ACACCTCCAGGTCCTTGCTGACTCCGGCCTGTTGAAAGGGAACGCCATGGTCCTGTGCTG	767
Qy	674	TGG--GGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCT	731
Db	768	TGGGAGTCCCAAGGAAGAGGCTCTCTTCTGGACAAACAACCTCCAAA--CCCAAGGCT	824
Qy	732	GTGCAAACACATGCCC	747
Db	825	GTGCCAACACATGCCC	840

RESULT 9

CF993841

LOCUS CF993841 838 bp mRNA linear EST 25-NOV-2003

DEFINITION AGENCOURT_15622657 NIH_MGC_147 Homo sapiens cDNA clone

IMAGE:30705878 5', mRNA sequence.

ACCESSION CF993841

VERSION CF993841.1 GI:38509901

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

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REFERENCE      1 (bases 1 to 838)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Daniela S. Gerhard, Ph.D.
                Office of Cancer Genomics
                National Cancer Institute / NIH
                Bldg. 31 Rm10A07 Bethesda, MD 20892
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Dr. Stefan Hansson
                cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
                and advice from Piero Carninci (RIKEN)
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: NDAM1068 row: d column: 15
                High quality sequence stop: 558.

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                    /clone_lib="NIH_MGC_147"
                    /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                    allI-XhoI; Site_2: BamH; Oligo-dT primed using primer
                    5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
                    insert size 2.3 kb and normalized to ROT 5. This is a
                    primary library enriched for full-length clones and
                    constructed using the Cap-trapper method (Carninci, in
                    preparation). Library constructed by M. Brownstein
                    (NIMH/NHGRI, National Institutes of Health). Note: This is
                    a NIH_MGC library."
```

ORIGIN

Query Match 61.9%; Score 545.4; DB 7; Length 838;
Best Local Similarity 98.9%; Pred. No. 7.6e-123;
Matches 549; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	327	GAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	386
Db	16	GCGTAGAACCAGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	75
Qy	387	AGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGCCTGCTCCAGCGCCCCGGCTTCAG	446

Db	76	AGCCTGAGGAGGTGTCTTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	135
Qy	447	GTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGC	506
Db	136	GTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGC	195
Qy	507	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	566
Db	196	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	255
Qy	567	TTCCAGAACAGTGTCTTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	626
Db	256	TTCCAGAACAGTGTCTTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	315
Qy	627	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGG	686
Db	316	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGG	375
Qy	687	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	746
Db	376	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	435
Qy	747	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTATAAGTTGT	806
Db	436	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTATAAGTTGT	495
Qy	807	TTTACAGATACGGAAACAGTCCAAAATGGGATTTATAAATTTCTTTTTTGCATTATAAATA	866
Db	496	TTTACAGATACGGAAACAGTCCAAAATGGGATTTATAAATTTCTTTTTTGCATTATAAATA	555
Qy	867	AAGATCCTCTGTAAC	881
Db	556	AAGATCCTCTGTAAC	570

RESULT 10

AA760709/c

LOCUS	AA760709	600 bp	mRNA	linear	EST 07-FEB-1998
DEFINITION	nz13c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287668 3', mRNA sequence.				
ACCESSION	AA760709				
VERSION	AA760709.1 GI:2809639				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.				

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FEATURES
    source          Location/Qualifiers
                    1. .600
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:1287668"
                    /tissue_type="germinal center B cell"
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_GCB1"
                    /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                    1st strand cDNA was prepared from human tonsillar cells
                    enriched for germinal center B cells by flow sorting
                    (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr.
                    David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA
                    synthesis was primed with a Not I - oligo(dT) primer
                    [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCTCATTTTTTTTTTTTTTTTTT-3'
                    ]. Double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Not I and cloned into the Not I
                    and Eco RI sites of the modified pT7T3 vector. Library
                    went through one round of normalization, and was
                    constructed by Bento Soares and M. Fatima Bonaldo."
```

Query Match 61.7%; Score 543.8; DB 1; Length 600;
Best Local Similarity 98.8%; Pred. No. 1.8e-122;
Matches 578; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

Qy 298 ACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCG 357
 |||
 Db 600 ACGGGCATGATGCTGCCGAGGGACTT-GGGAGCACAGTCTGGCTGGATGAGACAGGGTCG 542

Qy	358	TGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGC	417
Db	541	TGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGC	482
Qy	418	TGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGT	477
Db	481	TGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGT	422
Qy	478	GTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGC	537
Db	421	GTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGC	362
Qy	538	AGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGA	597
Db	361	AGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGA	302
Qy	598	GTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCG	657
Db	301	GTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCG	242
Qy	658	CCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCC	717
Db	241	CCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTNN	182
Qy	718	CAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGC	777
Db	181	C-CCCCCAGGGCTGTGCAAACACATGCCCCTCCCATAAGCACCAACAAGAACTTCTTGC	123
Qy	778	A-GGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGG	836
Db	122	AGGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGG	63
Qy	837	ATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	881
Db	62	ATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	18

RESULT 11
BQ025351/c
LOCUS BQ025351 573 bp mRNA linear EST 27-MAR-2002
DEFINITION UI-1-BB1p-aud-e-02-0-UI.s1 NCI_CGAP_P16 Homo sapiens cDNA clone
UI-1-BB1p-aud-e-02-0-UI 3', mRNA sequence.
ACCESSION BQ025351
VERSION BQ025351.1 GI:19760630
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 573)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-aud-e-02-0-UI"
/tissue_type="Placenta"
/dev_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_P16"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with
a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_P16 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGAA. For
additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG_TISSUE=placenta human full term
TAG_LIB=UI-1-BB1p
TAG_SEQ=AGGAA"

ORIGIN

Query Match 61.3%; Score 539.8; DB 4; Length 573;
Best Local Similarity 99.5%; Pred. No. 1.7e-121;
Matches 552; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	327	GAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	386
Db	569	GAGGACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	510
Qy	387	AGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	446
Db	509	AGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	450
Qy	447	GTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGC	506
Db	449	TTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGC	390
Qy	507	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	566
Db	389	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	330
Qy	567	TTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	626
Db	329	TTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	270
Qy	627	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGG	686
Db	269	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGG	210
Qy	687	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	746
Db	209	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	150
Qy	747	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTATAAGTTGT	806
Db	149	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTATAAGTTGT	90
Qy	807	TTTACAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATA	866
Db	89	TTTACAGATACGGAAACAGTCCAAAATGGGATTTATAA-TTCTTTTTTGCATTATAAATA	31
Qy	867	AAGATCCTCTGTAAC	881
Db	30	AAGATCCTCTGTAAC	16

RESULT 12

BQ025360/c

LOCUS BQ025360 581 bp mRNA linear EST 27-MAR-2002

DEFINITION UI-1-BB1p-aud-f-02-0-UI.s1 NCI_CGAP_P16 Homo sapiens cDNA clone
UI-1-BB1p-aud-f-02-0-UI 3', mRNA sequence.

ACCESSION BQ025360

VERSION BQ025360.1 GI:19760639

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 581)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers

source 1. .581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-aud-f-02-0-UI"
/tissue_type="Placenta"
/dev_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_P16"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with
a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_P16 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGAA. For
additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG_TISSUE=placenta human full term
TAG_LIB=UI-1-BB1p
TAG_SEQ=AGGAA"

ORIGIN

Query Match 61.3%; Score 539.8; DB 4; Length 581;
Best Local Similarity 99.5%; Pred. No. 1.7e-121;
Matches 552; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	327	GAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	386
Db	569	GAGGACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	510
Qy	387	AGCCTGAGGAGGTGTCTTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	446
Db	509	AGCCTGAGGAGGTGTCTTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	450
Qy	447	GTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGC	506
Db	449	TTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGC	390
Qy	507	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	566
Db	389	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	330
Qy	567	TTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	626
Db	329	TTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	270
Qy	627	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGG	686
Db	269	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGG	210
Qy	687	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	746
Db	209	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	150
Qy	747	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTATAAGTTGT	806
Db	149	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTATAAGTTGT	90
Qy	807	TTTACAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATA	866
Db	89	TTTACAGATACGGAAACAGTCCAAAATGGGATTTATAA-TTCTTTTTTGCATTATAAATA	31
Qy	867	AAGATCCTCTGTAAC	881
Db	30	AAGATCCTCTGTAAC	16

DEFINITION UI-E-CL1-afb-g-19-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
UI-E-CL1-afb-g-19-0-UI 5', mRNA sequence.

ACCESSION BM711587

VERSION BM711587.1 GI:19024845

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 591)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: Soares, MB
Cancer Biology & Epigenomics Program
Children's Memorial Research Center
2300 Children's Plaza, Box 220, Chicago, IL 60614-3394, USA
Tel: 773 755 6551
Fax: 773 755 6378
Email: mbsoares@childrensmemorial.org
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source 1..591
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CL1-afb-g-19-0-UI"
/tissue_type="human retina"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CL1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CL1 is a normalized cDNA library containing the
following tissue(s): retina. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac

Query Match 60.9%; Score 536.4; DB 4; Length 591;
Best Local Similarity 96.0%; Pred. No. 1.2e-120;
Matches 549; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

http://es/ScoreAccessWeb/GetItem.action?AppId=105295...7_122917_us-10-529-592a-1.rst&ItemType=4&startByte=0 (30 of 35)5/19/2009 9:51:32 AM

Db 560 TCTTTTTTGCATTTATAATANAGATCCTCTGT 591

RESULT 14

AI973037/c

LOCUS AI973037 539 bp mRNA linear EST 08-MAR-2000

DEFINITION wr46g08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2490782 3', mRNA sequence.

ACCESSION AI973037

VERSION AI973037.1 GI:5769863

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 539)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 768 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 458.

FEATURES Location/Qualifiers

source 1. .539

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2490782"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA
from the normalized library NCI_CGAP_Pr22 was prepared,

and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 60.8%; Score 536; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.5e-120;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	345	TGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCT	404
Db	539	TGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCT	480
Qy	405	GGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCT	464
Db	479	GGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCT	420
Qy	465	GCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTC	524
Db	419	GCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTC	360
Qy	525	AGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTC	584
Db	359	AGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTC	300
Qy	585	CAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTG	644
Db	299	CAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTG	240
Qy	645	GTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGAC	704
Db	239	GTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGAC	180
Qy	705	AAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAAC	764
Db	179	AAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAAC	120
Qy	765	AAGAACTTCTTGACAGGTGGAGTGGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACA	824
Db	119	AAGAACTTCTTGACAGGTGGAGTGGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACA	60
Qy	825	GTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAA	880
Db	59	GTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAA	4

CB993691

LOCUS CB993691 843 bp mRNA linear EST 01-MAY-2003

DEFINITION AGENCOURT_13624626 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30338285 5', mRNA sequence.

ACCESSION CB993691

VERSION CB993691.1 GI:30288211

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM364 row: 1 column: 06

High quality sequence stop: 408.

FEATURES Location/Qualifiers

source

1. .843

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30338285"

/tissue_type="pre-eclamptic placenta"

/lab_host="DH10B TonA"

/clone_lib="NIH_MGC_148"

/note="Organ: placenta; Vector: pBluescriptR; Site_1:

allI-XhoI; Site_2: BamH; Library is oligo-dT primed and
directionally cloned using primer

5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 60.2%; Score 530.2; DB 7; Length 843;
 Best Local Similarity 92.5%; Pred. No. 4.2e-119;
 Matches 580; Conservative 0; Mismatches 43; Indels 4; Gaps 2;

Qy	6	ATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGACCGCCG	65
Db	28	ATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGACCGCCG	87
Qy	66	CCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGCAGTGA	125
Db	88	CCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGCAGTGA	147
Qy	126	GCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCCTGCCT	185
Db	148	GCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCCTGCCT	207
Qy	186	GAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCT	245
Db	208	GAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCT	267
Qy	246	GAACGACAAGCACCTGGACGTGCCCCGACATCATCATCACGCCCCCACCCCCACGGGCAT	305
Db	268	GAACGACAAGCACCTGGACGTGCCCCGACATCATCATCACGCCCCCACCCCCACGGGCAT	327
Qy	306	GATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGA	365
Db	328	GATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGA	387
Qy	366	TGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCT	425
Db	388	TGATGGAGAAATTGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCCGGCTGGCTCCT	447
Qy	426	GCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAA	485
Db	448	GCTCCAGCGGCTCGGCTTCAGGTGTCCGGCGGCGTGGCTGCCTGGACCAGGCGTGCTGGA	507
Qy	486	TACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAG	545
Db	508	TACCCTGGATGGGAACTGAGCGAACCTGGGCCTCCGCTCATAGAGACGTGTCAGGGACGT	567
Qy	546	CGAGGAATCCAG-CCTGTCCACTTCCAGAACAGTGTTTCCCAGG---CCCCGCTGAGTGG	601
Db	568	GTAGGGATCCAGCCCTGTTCCCCTTTTAAACAGCTTTTCCCCGGTGCCCTCCTTTATGGA	627
Qy	602	ACCGGACCTCTGACACCTCCAGGTTCT	628
Db	628	CCGGAACCTCCGAAACCTCCCCGTTT	654

Search completed: April 28, 2009, 04:48:02

Job time : 1887 secs

SCORE 8.6